

REMARKS

1. Amendments to the Claims

Claims 1, 3, and 4 have been amended to recite 95% sequence identity. Support for this amendment is found in the specification at page 36, line 18.

Claim 3 has been amended to recite "hybridization conditions of 0.1 x SSC to 0.2 x SSC at about 60-65 °C and/or washing conditions of 0.2 x SSC, 0.1% SDS at about 65-68 °C." Support for this amendment is found in the specification at page 41, lines 4-7.

Claims 5-13 have been canceled.

Claim 14 has been added. Support for claim 14 is found in claim 3 as filed.

Claim 15 has been added. Support for claim 15 is found in claim 1 as filed, and in the specification page 1, lines 6-7, and page 2, lines 9-11.

No new matter has been added.

2. Election/Restriction

Applicants note that the Examiner agreed to rejoin SEQ ID NOs: 69-74 and 80-85 to SEQ ID NO: 27 and SEQ ID NO: 75.

3. Objections to the Specification

The Examiner objects to the use of ExTaq™ and MetaPhor™ because they should be capitalized wherever they appear and be accompanied by the generic terminology.

Applicants submit that it is clear from the descriptions in the specification together with the common knowledge in the art that ExTaq™ is a DNA polymerase and MetaPhor™ is an agarose gel. (*See e.g.*, Specification, page 67, lines 11-24, describing a DNA amplification reaction, and

page 79, lines 15-18, describing agarose gels). Both expressions are marked as trademarks already. Applicants submit that no amendment of the specification is needed.

4. Claim Rejections

4.1 35 U.S.C. §112 Indefiniteness

The Examiner rejects claims 3 and 4 as indefinite, stating “the recitation ‘moderate or high’ renders the claim indefinite. The recitation is a relative term with no defined meaning.” Applicants submit that the recitation has been amended to recite “under hybridization conditions of 0.1 x SSC to 0.2 x SSC at about 60-65 °C and/or washing conditions of 0.2 x SSC, 0.1% SDS at about 65-68 °C.” Applicants submit that the claim as amended is definite and request that the Examiner withdraw the rejection.

Applicants also point out that the recitation in claim 3(o) is a condition of high stringency.

4.2 35 U.S.C. §112 Written Description

The Examiner rejects claims 1, 3, and 4 for lack of adequate written description. The Examiner states that “[t]he applicants do not identify any essential regions of the protein of SEQ ID No: 75” or a sequence having 70% sequence identity to bases 215-2587 of SEQ ID NO: 69. Applicants respectfully traverse.

Applicants first note that the percent identity of the amino acid sequences is now 95%. Applicants submit that the disclosure of SEQ ID NO: 75 combined with the pre-existing knowledge in the art regarding the genetic code and its redundancies would have put one of skill in possession of the genus of nucleic acids that encode SEQ ID NO: 75. Thus Applicants submit that the disclosure would have indicated to one of skill in the art that Applicants were in possession of the claimed genus of nucleic acids encoding SEQ ID NO: 75 at the time of filing.

Furthermore, Applicants also submit that the specification, in combination with one of skill in the art, provides sufficient written description for a nucleic acid sequence encoding an amino

acid sequence having 95% identity to SEQ ID NO: 75. The specification provides the following guides for one skilled in the art: 1) it discloses a definition for “amino acid variation” on page 36, lines 10-20, and 2) it discloses conservative amino acid substitutions on page 42, lines 10-27. Furthermore, one of skill would use computer aided techniques, conventional sequencing, and nucleic acid synthesis to generate and identify nucleic acids that encode any polypeptide having 95% identity to SEQ ID NO: 75.

Additionally, Applicants submit that there is sufficient written description for the nucleotide sequence having 95% sequence identity to bases 215-2587 of SEQ ID NO: 69, nucleic acids which hybridize to the bases 215-2587 of SEQ ID NO: 69, and variants of the bases of 215-2587 of SEQ ID NO: 69. One of skill in the art would know that applicant was in possession of sequences having at least 95% sequence identity to bases 215-2587 of SEQ ID NO: 69 through computer aided analysis and sequencing.

Furthermore, there is sufficient written description for nucleic acids which hybridize to the bases 215-2587 of SEQ ID NO: 69 in “hybridization conditions of 0.1 x SSC to 0.2 x SSC at about 60-65 °C and/or washing conditions of 0.2 x SSC, 0.1% SDS at about 65-68 °C” because hybridization under highly stringent conditions requires a high degree of structural complementarity, and thus share many nucleotides in common with the bases 215-2587 of SEQ ID NO: 69. Therefore, the disclosure of bases 215-2587 of SEQ ID NO: 69 combined with knowledge in the art regarding hybridization would put one in possession of the genus of nucleic acids that would hybridize to the bases 215-2587 of SEQ ID NO: 69 under the claimed conditions. Therefore, Applicants submit that the hybridization is sufficiently described. Applicants respectfully request that the rejection be withdrawn.

Applicants submit that the specification has sufficient written description for variants of bases 215-2587 of SEQ ID NO: 69 that encode the amino acid sequence of SEQ ID NO: 75 because due to the degeneracy of the genetic code, one skilled in the art is aware that only a limited number of codons can encode a specific amino acid, and that the genetic code provides a known

correlation between codon function (encoding a specific amino acid) and each codon structure. Furthermore, because one of skill would be able to envision all the nucleotide sequences encoding SEQ ID NO: 75 or an amino acid sequence with 70% identity to SEQ ID NO: 75 (now 95% identity), variant sequences of bases 215-2587 of SEQ ID NO: 69 as described in the present specification are included in that genus.

Additionally, Applicants submit that the structure of the RF-1 protein was known, at least in part. One of skill would have recognized its sequence identity with the repeated PPR motif in the central region of the protein. The PPR motif is disclosed in Small et al., *The PPR motif – a TPR-related motif prevalent in plant organellar proteins*, Trends in Biochemical Science, 2000 Feb.;25(2), 46-7. Furthermore, the specification discloses that the N-terminal amino acid sequence would have been considered necessary so that the Rf-1 protein is translocated to mitochondria wherein the RF-1 protein functions. (See specification, page 145, lines 16-25).

Thus Applicants submit that there is sufficient written description for the claimed methods and request the Examiner withdraw the rejection.

4.3 Enablement

The Examiner rejects claims 1, and 3-4, alleging that the specification does not reasonably provide enablement for any nucleotide sequence which encodes an amino acid sequence having at least 70% sequence identity to the amino acid sequence of SEQ ID NO: 75, or sequence identity to bases 215-2587 of SEQ ID NO: 69.

Applicants submit that one skilled in the art would be able to make and use a polypeptide having 95% sequence identity to SEQ ID NO: 75, based on the disclosure of the specification and knowledge in the genetic code, discussed above. Additionally, one of skill would be able to make the present invention because the specification discloses how to make the claimed sequences, screen the sequences, create a plasmid encoding the Rf-1 promoter region and the Rf-1 translation region, transform E. coli with the plasmid, create a triparental mating with

agrobacterium tumefaciens and helper E. coli, and transform MS Koshihikari. (Specification, Examples 15 and 16, pages 143-150). The specification then discloses how to grow the transformed plants and test seed fertility. *Id.* Thus Applicants disclose how to make nucleic acids useful in the method of the claimed invention.

As to the need for the reverse complement of a sequence “hybridizing to” a recited reference sequence, the Examiner should consider that the claim recites the transitional term “comprising” and is inclusive of a double stranded nucleic acid.

Applicants submit that the present application is enabled based on the specification and the knowledge of those skilled in the art. Applicants request that the Examiner withdraw the rejection.

4.4 35 U.S.C. §102 Anticipation

The Examiner rejects claims 1 through 3 under 35 U.S.C. §102 as being anticipated by Hanson et al. (US Patent No. 7,164,058) (hereinafter D1). Applicants respectfully traverse.

Applicants submit that D1 does not anticipate every element of the claimed invention. Applicants highlight that the claims now recite sequences having 95% identity to amino acid sequence SEQ ID NO: 75. D1 describes a method for restoring fertility to the cytoplasmic male sterile *Petunia* plant by introducing the *Petunia* Rf-PPR592 gene. D1 also discloses a nucleic acid sequence of SEQ ID NO: 22 derived from rice, which is a rice homolog of the *Petunia* Rf-PPR592 gene.

Applicants submit that the rice gene of SEQ ID NO: 22 in D1 is only 87.6% identical to SEQ ID NO: 69 disclosed in the present application. The amino acid sequence SEQ ID NO: 23 encoded by SEQ ID NO: 22 has only 84.4% identity to SEQ ID NO: 75 of the present application. Applicants submit that the present sequences can be distinguished, because the present application requires that the claimed sequences have 95% identity to the amino acid sequence of

SEQ ID NO: 75 or the nucleic acid sequence of SEQ ID NO: 69. Thus Applicant submits that the present invention is not anticipated by D1.

Furthermore, D1 does not provide any experimental evidence that the rice gene of SEQ ID NO: 22 or the rice protein of SEQ ID NO: 23 restores fertility to a rice plant. It is now generally recognized by those skilled in the art that the genes for causing cytoplasmic male sterility and the genes for restoring fertility have a specific relationship. These genes and their relationship largely vary depending on a kind of plant, and the specific type of male sterility. D1 seems to provide experimental results for *Petunia*, but this does not guarantee success in restoring fertility in the rice plant by using the nucleic acid sequence SEQ ID NO: 22.

At least with respect to claim 15, the Rf-1 gene of the present invention seems to be effective principally due to the rice **BT** type cytoplasmic male sterility. Tada et al., Breeding Science, 2007 vol. 57; 223-29, describes that Rf-1 exhibited poor activity in restoring fertility to the rice of the **WA** type cytoplasmic male sterility. From this teaching, the sequences of the present invention may only poorly restore the **WA** type cytoplasmic male sterility of the rice, whereas they have shown activity in restoring the **BT** type of cytoplasmic male sterility. On the other hand, the sequences disclosed in the present invention, and their variations, may have either high or low activity against the **WA** type cytoplasmic male sterility, it is unclear. Thus Applicants submit that the teachings of the sequences in D1 to restore cytoplasmic male fertility do not guarantee activity against the **BT** type cytoplasmic male fertility like those of the present invention.

Therefore, Applicants suggest that reference D1, Hanson et al., does not anticipate every element of the claimed invention. Applicants respectfully request the Examiner withdraw the rejection.

CONCLUSION

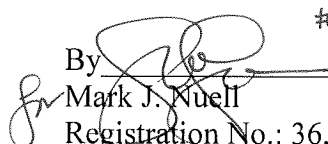
Applicants request the Examiner review the file and withdraw the present rejections.

Should there be any outstanding matters that need to be resolved in the present application, the Examiner is respectfully requested to contact Mark J. Nuell Reg. No. 36,623 at the telephone number of the undersigned below, to conduct an interview in an effort to expedite prosecution in connection with the present application.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies to charge payment or credit any overpayment to Deposit Account No. 02-2448 for any additional fees required under 37.C.F.R. §§1.16 or 1.14; particularly, extension of time fees.

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Respectfully submitted,

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